



2/17

```

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80| 90| 100| 110| 120| 130| 140|

1fm9AA00 -----
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80| 90| 100| 110| 120| 130| 140|

1fm9AA00 -----
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150| 160| 170| 180| 190| 200| 210|

1fm9AA00 -----
nedmpvERILEAE LAVEPKTETTYVEANMGLNPSSPNDEPV
10| 20| 30| 40|
:....: . . . . :
egesytlavevaliglggrimpdglytqekvcrneEQ LISKLOEIEIDDTLVKIFRKQAVELLEAGPY
220| 230| 240| 250| 260| 270| 280|

1fm9AA00 -----
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50| 60| 70| 80| 90| 100| 110|
: . . . . :
SGLGEIITHRESVPMHTFAKYL--FTSLPHD-AELAYKTALRAMRLLVLESTAPSGDLTRPHHIASVVPN
290| 300| 310| 320| 330| 340| 3

1fm9AA00 -----
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Figure 2 Part I

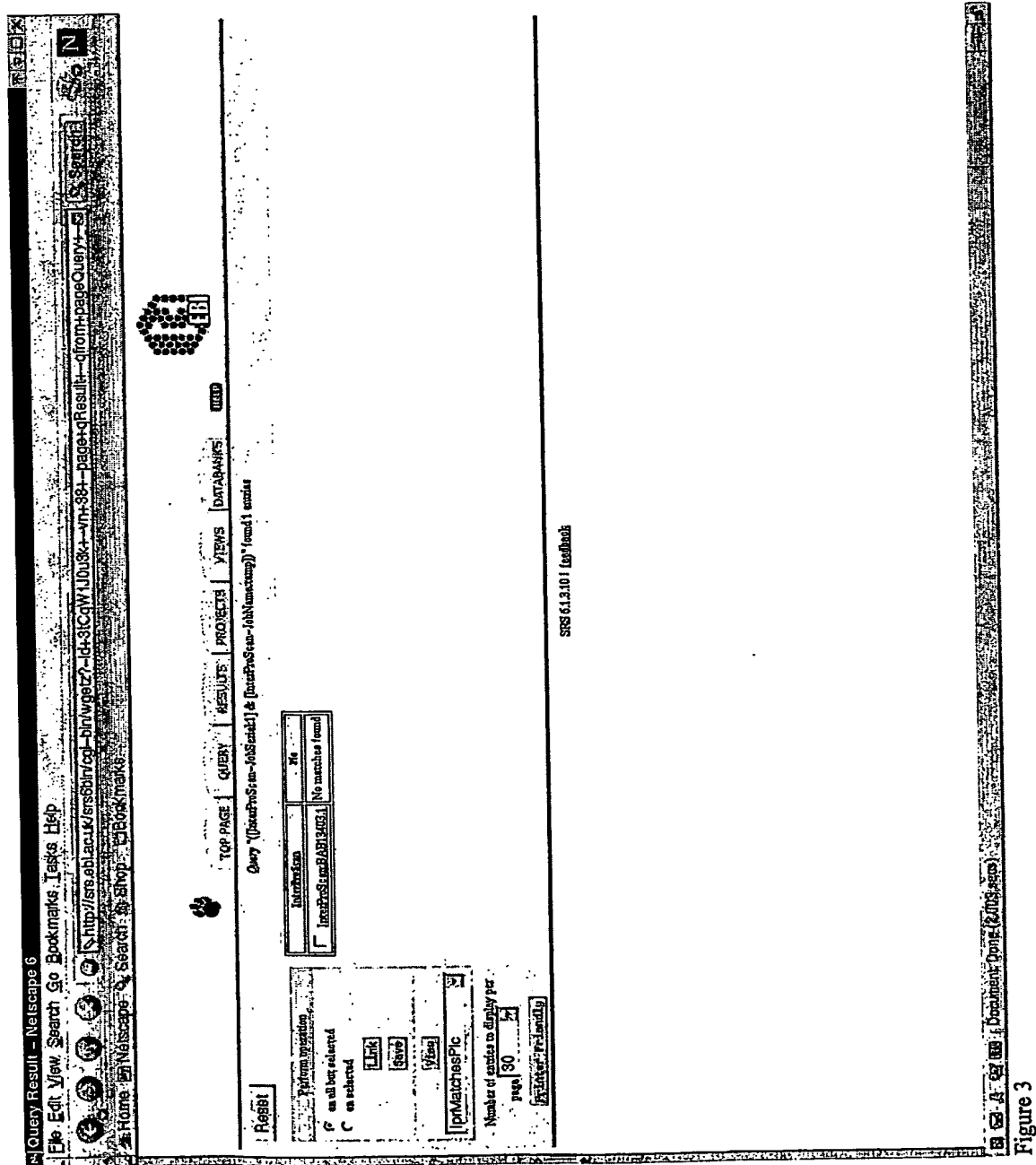
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70| 480| 490| 500| 510| 520| 530|
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BAB13403 hslgknelaaiplvvksvkatvlsdillrrctlttpgmvglhgrrnsgklmsldkaplrqlldatigay 6
10| 620| 630| 640| 650| 660| 670|
1fm9AA00 -----
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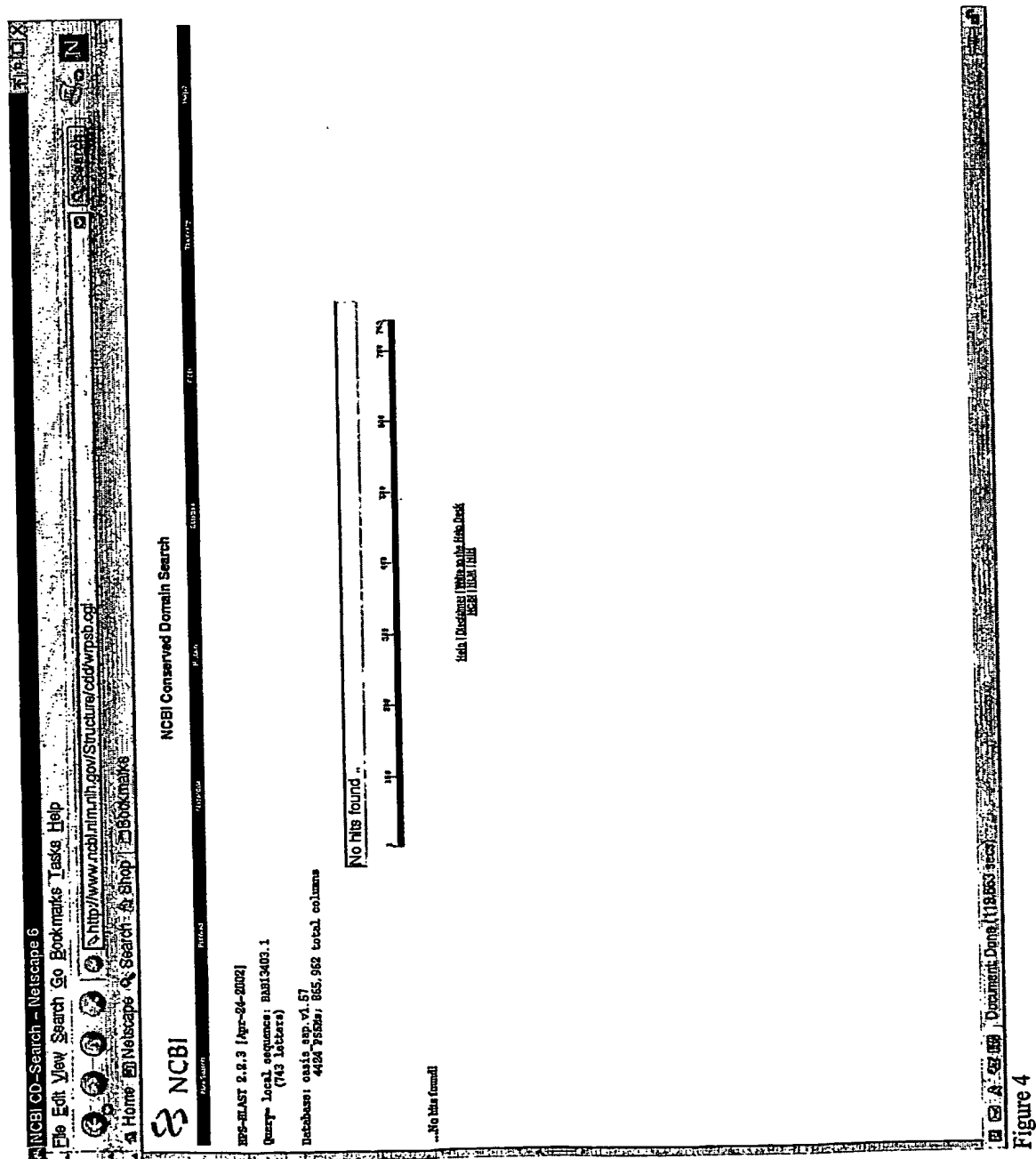
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Figure 2 Part II

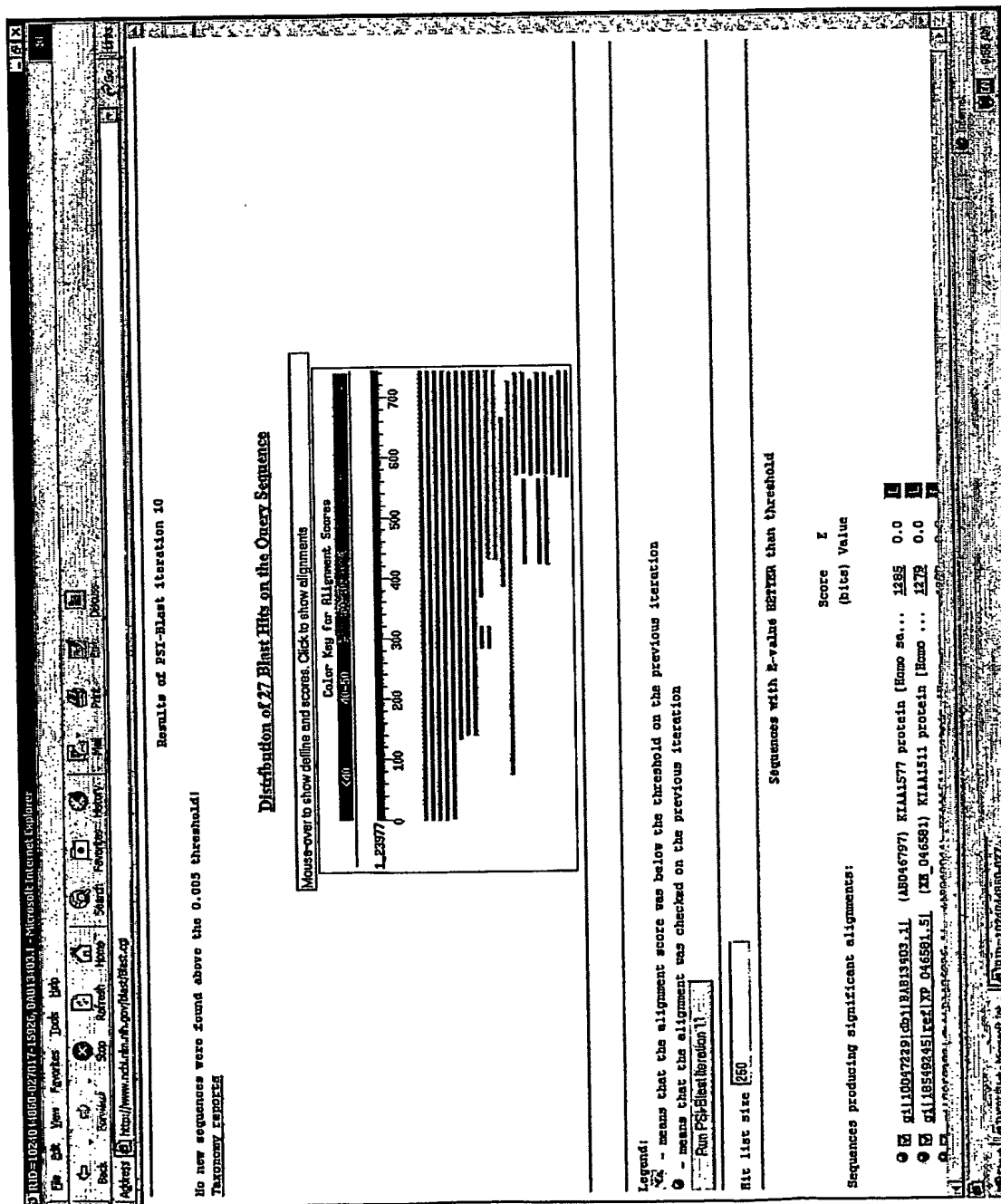
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NCBI Sequence Viewer - Nelscape 6
 File Edit View Search Go Bookmarks Tasks Help
 http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=protein&list_uids=10047229&type=GenPept
 Home Nelscape 6 Search 6 Shop 6 Bookmarks 6
 NCBI Protein
 Display default Save Text Add to clipboard Go Clear
 F:10047229 KIAA1577 protein [4:10047229] Linear PRI 22-FEB-2001

LOCUS BAB13403 743 aa
 DEFINITION KIAA1577 protein [Homo sapiens].
 ACCESSION BAB13403
 VERSION BAB13403.1 01:10047229
 DISCUSSION Locus AB046797 accession AB045751.4
 KEYWORDS
 SOURCE human
 ORGANISM Homo sapiens
 Chordata; Echinodermata; Vertebrata; Euteleostomi; Mammalia; Primates; Hominidae; Homo.
 1 (cds)
 Nagase T., Kikuno R., Nakayama M., Hirosewa M. and Ohara O.
 Prediction of the coding sequences of unidentified human genes.
 XVIII. The complete sequences of 100 new cDNA clones from brain
 which code for large proteins in vitro
 DNA Res. 7 (4), 271-281 (2000)
 JOURNAL JOURNAL OF BIOCHEMICAL PHYSIOLOGY
 PUBMED 10971871
 REFERENCES Ohara O., Nagase T. and Kikuno R.
 Prediction of the coding sequences of unidentified human genes.
 XVIII. The complete sequences of 100 new cDNA clones from brain
 which code for large proteins in vitro
 Submitted (03-JUN-2000) Osaka University, Osaka University
 Department of Human Gene Research, 152-3, Yama, Kasugan, Chiba
 258-0812, Japan (E-mail: ohara@ohara.osaka-u.ac.jp)
 URL: http://www.kazusa.or.jp/huge, Tel: 81-438-52-3913,
 Fax: 81-438-52-3914
 Location/Qualifiers
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 121 aacgagcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc
 181 aacgagcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc
 241 aacgagcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc
 301 aacgagcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc
 361 aacgagcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc
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 601 aacgagcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc
 661 aacgagcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc cggcggcgc
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Figure 7

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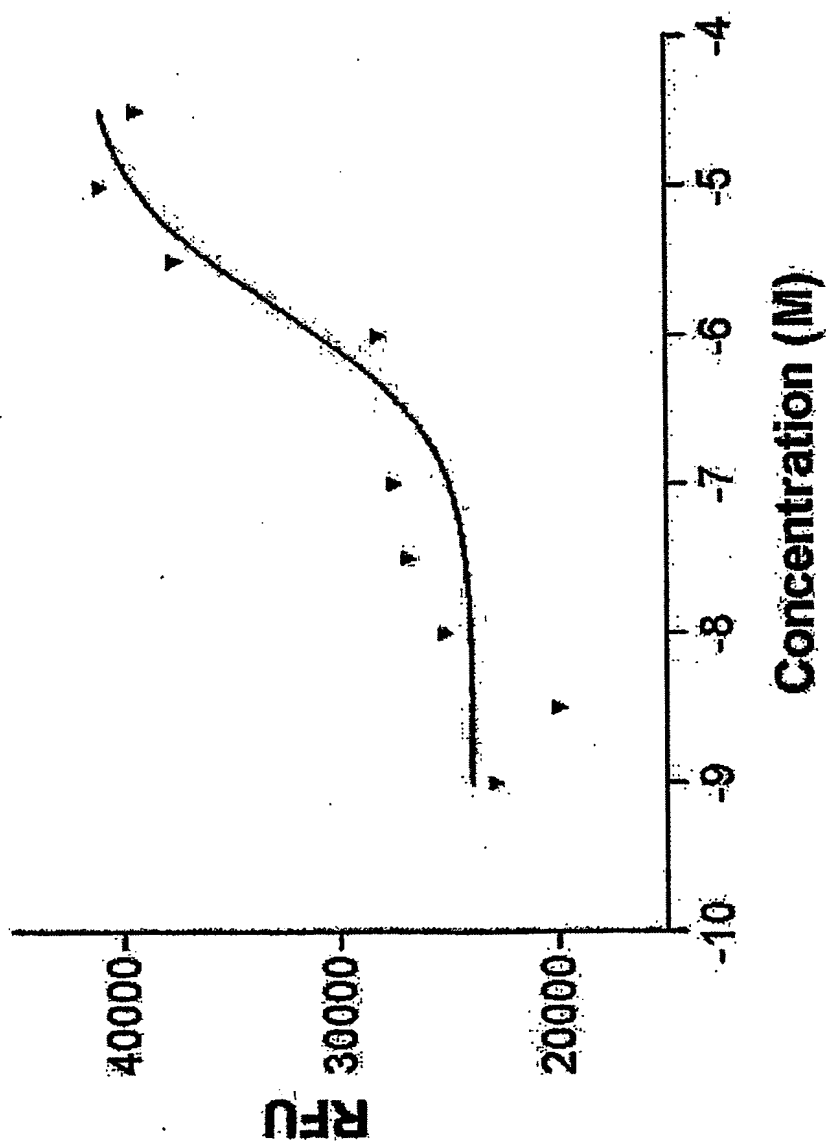
Dose response LBDG14 agonist # 1

Figure 8

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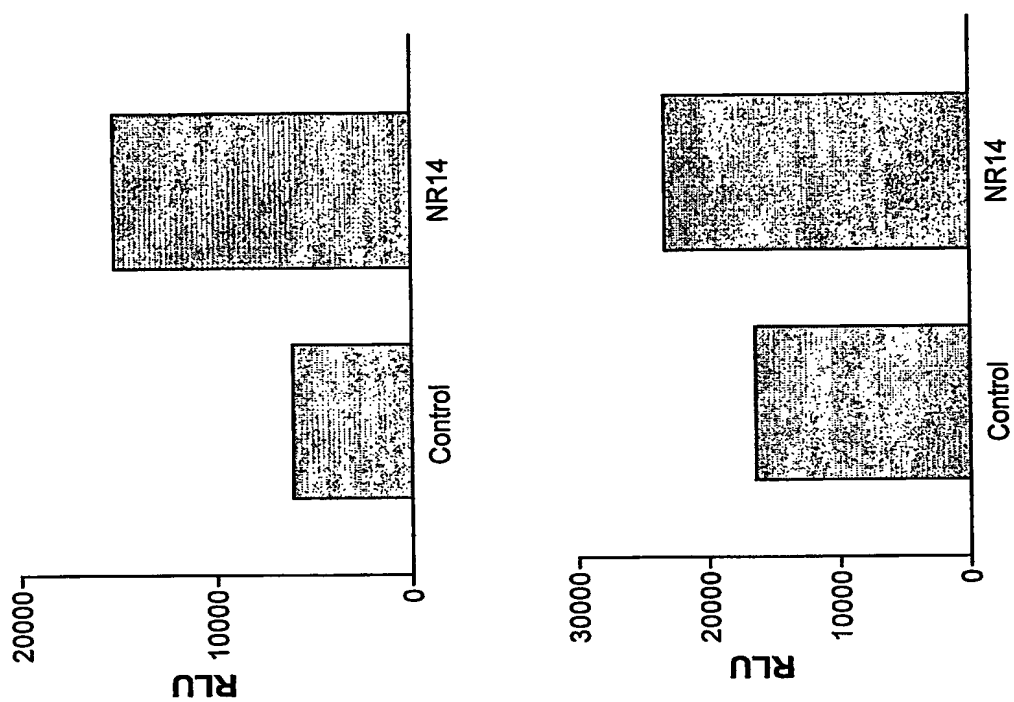


Figure 9

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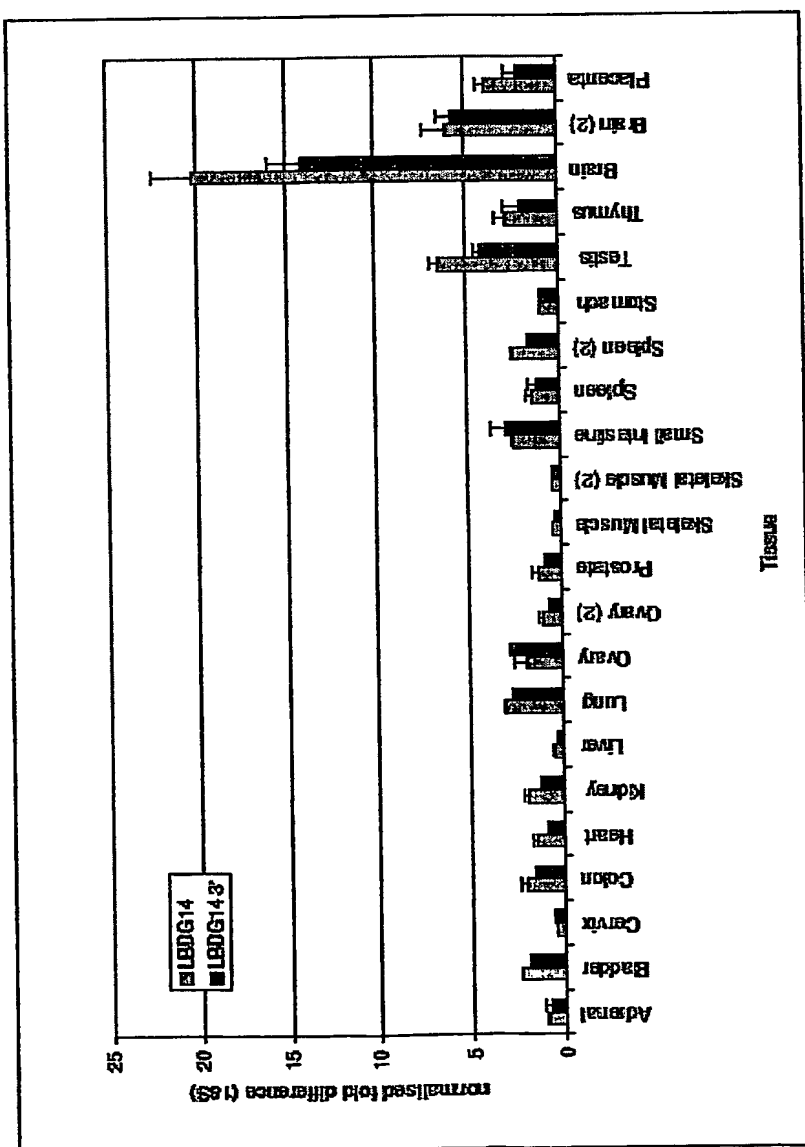


Figure 10

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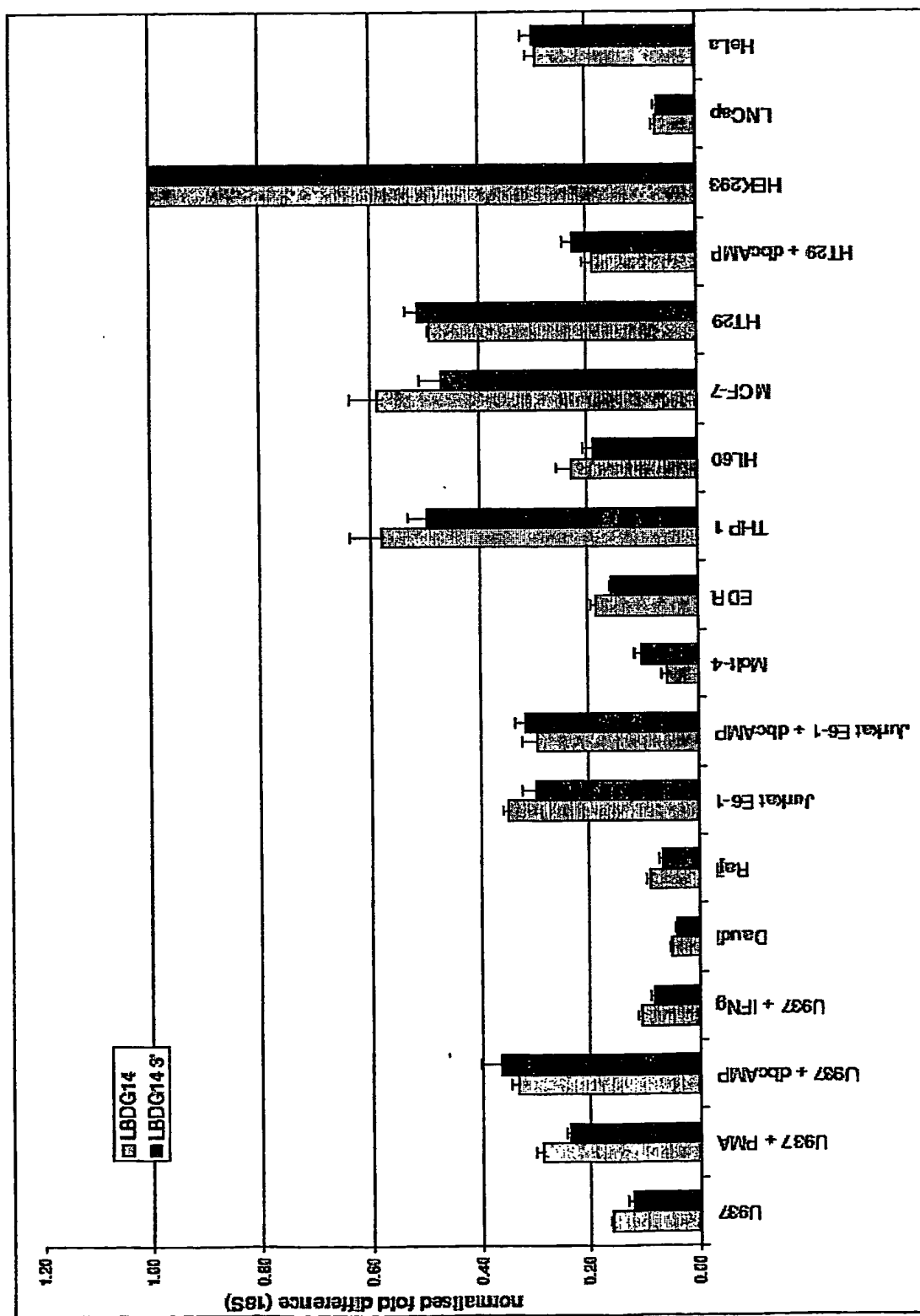


Figure 11

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NR14 Gene Expression in Normal Tissues (Probe Set 226208_at)

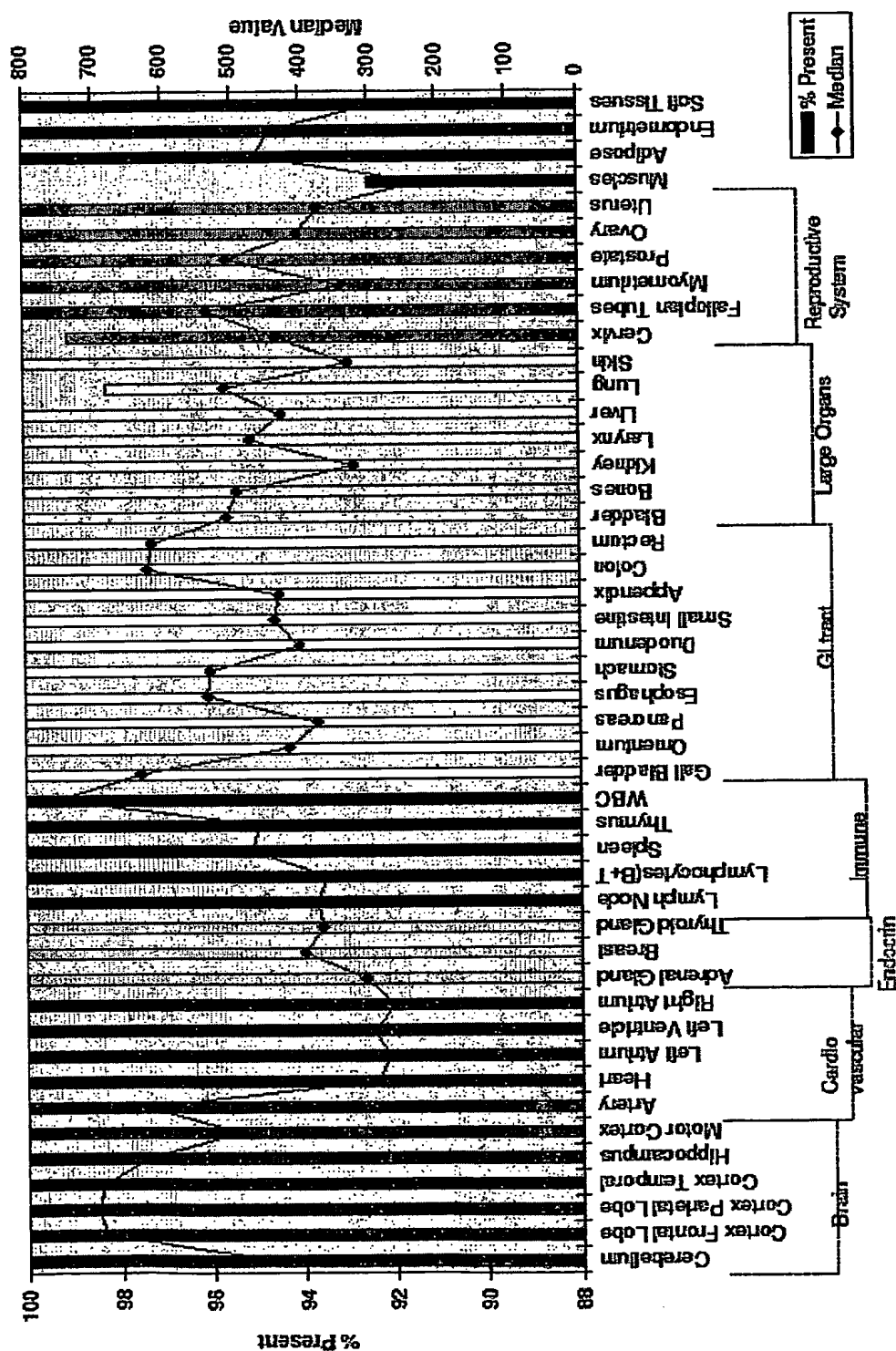


Figure 13

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Fig. 14

Affy ID	Tissue	Disease	Morphology	Mean fluorescent units for control samples	SD for controls	Number of controls	CPC%	Mean fluorescent units for disease samples	SD for disease samples	Number of disease samples	EPC%	Fold Change Disease compared to control	T-Stat
226208_at	Soft tissues, nos	Benign neoplasm of connective and other soft tissues, nos	Schwannoma, nos	446.47	235.79	6	100	1179.7	382.38	7	100	2.64	4.22
226208_at	Lung, nos	Malignant neoplasm of lung, nos	Neuroendocrine carcinoma	527.78	171.91	113	100	293.01	36.84	3	100	-1.8	-8.79
226208_at	Lung, nos	Secondary malignant neoplasm of lung, nos	Squamous cell carcinoma, nos	527.78	171.91	113	100	276.16	38.13	3	100	-1.91	-9.21
226208_at	Stomach, nos	Malignant neoplasm of stomach, nos	Sarcoma, nos	567.17	182.9	53	100	972.59	400.57	8	100	1.72	2.82
226208_at	Small Intestine, nos	Malignant neoplasm of small Intestine, nos	Sarcoma, nos	453.79	139.29	81	100	1074.08	303.6	4	100	2.37	4.07
226208_at	Small Intestine, nos	Malignant lymphoma, nos of unspecified, extranodal or solid organ site	Malignant lymphoma, nos	453.79	139.29	81	100	272.87	117.85	7	85.71	-1.66	-3.84
226208_at	Colon, nos	Secondary malignant neoplasm of colon, nos	Adenocarcinoma, nos	632.74	157.12	188	100	358.15	99.67	3	100	-1.77	-4.68
226208_at	Colon, nos	Malignant lymphoma, nos of unspecified, extranodal or solid organ site	Malignant lymphoma, nos	632.74	157.12	188	100	267.11	60.47	3	100	-2.37	-8.95
226208_at	Kidney, nos	Malignant neoplasm of kidney, nos	Wilms' tumor	354.18	120.42	94	100	671.87	95.69	8	100	1.9	8.81
226208_at	Kidney, nos	Benign neoplasm of kidney, nos	Oncocytoma	354.18	120.42	94	100	583.81	276.66	10	100	1.65	2.6
226208_at	Testis, nos	Malignant neoplasm of testis, nos	Seminoma, nos	388.96	109.77	8	100	254.38	105.58	8	87.5	-1.53	-2.5
226208_at	Neutrophils		Activated neutrophils (Versinia)	1736.4	1083.98	5	100	3897.07	679.19	7	100	2.24	3.94

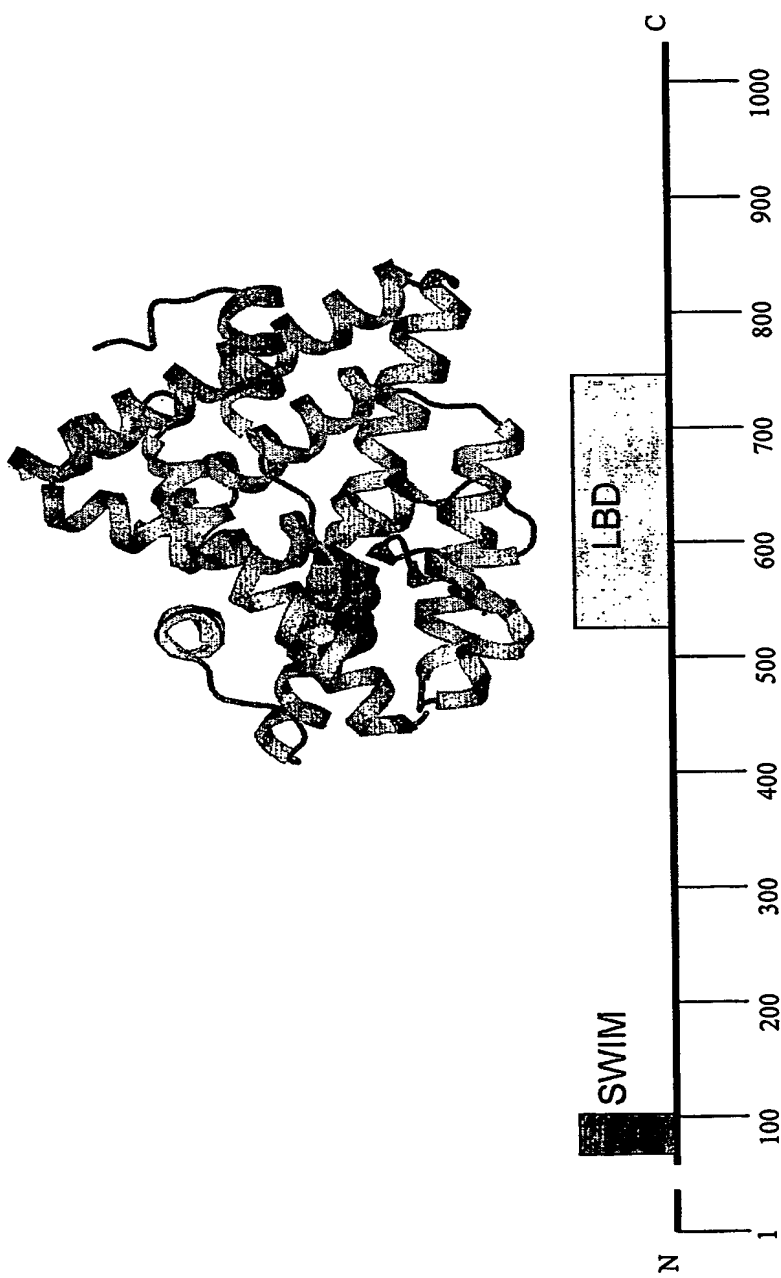


Figure 15

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Figure 16: Alignment of original sequence prediction (SEQ ID NO: 2) with the extend d sequence prediction (SEQ ID NO: 32)

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LBDG14_FL      VTCSCGNKIDIFYCAHVVALSLYRIRKPDQVKLHLPISSETLFQMNRDQLQKFVQYLITVHH 120
BAB13403.1      -----
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LBDG14_FL      TEVLPTAQLADEILSQNSEINQVHGAPDPTAGASIDDENCWHLDEEQVQEQVKLFLSQG 180
BAB13403.1      -----
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BAB13403.1      -----
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LBDG14_FL      LWDELGALWMCIVLNPHCKLEQKASWLKQLKKWNSVDVCPWEDGNHGSSELPNLTNALPQG 300
BAB13403.1      -----NSVDVCPWEDGNHGSSELPNLTNALPQG 27
                .. :. : . . . . :.:.. :. . . *****
LBDG14_FL      ANANQDSSNRPHRTVFTRAIEACDLHWQDHLQHISSDLYTNYCYHDDTENSIFDSRGW 360
BAB13403.1      ANANQDSSNRPHRTVFTRAIEACDLHWQDHLQHISSDLYTNYCYHDDTENSIFDSRGW 87
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LBDG14_FL      PLWHEHVPTACARVDALRSHGYPREALRLAIAIVNTLRRQQQKQLEMFRTOQKELPHKNI 420
BAB13403.1      PLWHEHVPTACARVDALRSHGYPREALRLAIAIVNTLRRQQQKQLEMFRTOQKELPHKNI 147
                *****
LBDG14_FL      TSITNLEGWVGHPLDPVGTLFSSLMACRIDDENLSGFSDFTENMGQCKSLEYQHLPAHK 480
BAB13403.1      TSITNLEGWVGHPLDPVGTLFSSLMACRIDDENLSGFSDFTENMGQCKSLEYQHLPAHK 207
                *****
LBDG14_FL      FLEEGESYLTAVEVALIGLGQQRIMPDLGYTQEKVCRNEEQLSKLEIQLDDTLVKIF 540
BAB13403.1      FLEEGESYLTAVEVALIGLGQQRIMPDLGYTQEKVCRNEEQLSKLEIQLDDTLVKIF 267
                *****
LBDG14_FL      RKQAVFLLLEAGPYSGLGEIITHRESVPMHTFAKYLFSTLLPHDAELAYKIALRAMRLLVLE 600
BAB13403.1      RKQAVFLLLEAGPYSGLGEIITHRESVPMHTFAKYLFSTLLPHDAELAYKIALRAMRLLVLE 327
                *****
LBDG14_FL      STAPSGDLTRPHHIASVVPNRYPRWFTLSHIESQQCELASTMTLTAAGDVRRLLETVLESI 660
BAB13403.1      STAPSGDLTRPHHIASVVPNRYPRWFTLSHIESQQCELASTMTLTAAGDVRRLLETVLESI 387
                *****
LBDG14_FL      QKNIHSSSHIFKLAQDAFKIATLMDSLPDITLLKVSLELGLQVMRMTLSTLNWRRREMVR 720
BAB13403.1      QKNIHSSSHIFKLAQDAFKIATLMDSLPDITLLKVSLELGLQVMRMTLSTLNWRRREMVR 447
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LBDG14_FL      WLVTCAVEGVYALDSIMQWFTLFTPTAETSIVATTVMNSTIVRLHLDCHQEQKCLASS 780
BAB13403.1      WLVTCAVEGVYALDSIMQWFTLFTPTAETSIVATTVMNSTIVRLHLDCHQEQKCLASS 507
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LBDG14_FL      ARTLALQCAMKDPQNCALSALTLCCKDHIAFETAYQIVLDAATTGMSYQLFTIARYMEH 840
BAB13403.1      ARTLALQCAMKDPQNCALSALTLCCKDHIAFETAYQIVLDAATTGMSYQLFTIARYMEH 567
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LBDG14_FL      RGYPMRAYKLATLAMTHLNLSYNQDTHPAINDVLWACALSHSLGKNELAAIPLVVKSVK 900
BAB13403.1      RGYPMRAYKLATLAMTHLNLSYNQDTHPAINDVLWACALSHSLGKNELAAIPLVVKSVK 627
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LBDG14_FL      CATVLSLILRRCTLTTPGMVGLHGRNSGKLSLMDKAPLRQLLDATIGAYINTTHSRRLTH 960
BAB13403.1      CATVLSLILRRCTLTTPGMVGLHGRNSGKLSLMDKAPLRQLLDATIGAYINTTHSRRLTH 687
                *****
LBDG14_FL      ISPRHYSEFIEFLSKARETFLMAHDGHIQFTQFIDNLKQIYKGKKKLMMLVRERFG 1016
BAB13403.1      ISPRHYSEFIEFLSKARETFLMAHDGHIQFTQFIDNLKQIYKGKKKLMMLVRERFG 743
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